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RAW SEQUENCE LISTING   DATE: 11/01/2001
PATENT APPLICATION: US/09/877,987   TIME: 14:39:11

Input Set : A:\Townsen1.app
Output Set: N:\CRF3\11012001\I877987.raw   **ENTERED**

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 3 <110> APPLICANT: Townsend, Robert M.
 4        Todderud, Charles G
 5        Peach, Robert J.
 7 <120> TITLE OF INVENTION: METHODS FOR REGULATING A CELL-MEDIATED IMMUNE RESPONSE
 8        BY BLOCKING LYMPHOCYTIC SIGNALS AND BY BLOCKING LFA-1
 9        MEDIATED ADHESION
11 <130> FILE REFERENCE: D0009NP/30436.53USU1
13 <140> CURRENT APPLICATION NUMBER: 09/877,987
14 <141> CURRENT FILING DATE: 2001-06-08
16 <150> PRIOR APPLICATION NUMBER: 60/210,671
17 <151> PRIOR FILING DATE: 2000-06-09
19 <160> NUMBER OF SEQ ID NOS: 9
21 <170> SOFTWARE: PatentIn Ver. 2.1
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25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
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30 cagcc                                                            65
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53 <211> LENGTH: 41
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55 <213> ORGANISM: Artificial Sequence
57 <220> FEATURE:
58 <223> OTHER INFORMATION: Description of Artificial Sequence:Oncostatin M
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66 <211> LENGTH: 42
67 <212> TYPE: DNA
68 <213> ORGANISM: Artificial Sequence
70 <220> FEATURE:
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 71 <223> OTHER INFORMATION: Description of Artificial Sequence:Oncostatin M
 72       CTLA4 (OMCTLA4) Reverse Primer
 74 <400> SEQUENCE: 5
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 79 <211> LENGTH: 1152
 80 <212> TYPE: DNA
 81 <213> ORGANISM: Artificial Sequence
 83 <220> FEATURE:
 84 <223> OTHER INFORMATION: Description of Artificial Sequence:CTLA4Ig
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 87 atgggtgtac tgctcacaca gaggacgctg ctcagtctgg tccttgcact cctgtttcca 60
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 89 ggcatcgcta gctttgtgtg tgagtatgca tctccaggca aagccactga ggtccgggtg 180
 90 acagtgcttc ggcaggctga cagccaggtg actgaagtct gtgcggcaac ctacatgatg 240
 91 gggaatgagt tgaccttcct agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
 92 gtgaacctca ctatccaagg actgaggggc atggacacgg gactctacat ctgcaaggtg 360
 93 gagctcatgt acccaccgcc atacacctg ggcataggca acggaaccca gatttatgta 420
 94 attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
 95 acatccccac cgtccccagc acctgaactc ctgggtggat cgtcagtctt cctcttcccc 540
 96 ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 600
 97 gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 660
 98 cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg ggtggtcagc 720
 99 gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 780
100 aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
101 gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 900
102 ctgacctgcc tggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960
103 gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1020
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110 <211> LENGTH: 383
111 <212> TYPE: PRT
112 <213> ORGANISM: Artificial Sequence
114 <220> FEATURE:
115 <223> OTHER INFORMATION: Description of Artificial Sequence:CTLA4Ig
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122              20                  25                  30
124 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
125          35                  40                  45
127 Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
128      50                  55                  60
130 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
131  65                  70                  75                  80
133 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
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134                    85                  90                  95
136 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
137               100                 105                 110
139 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
140               115                 120                 125
142 Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
143           130                 135                 140
145 Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
146 145               150                 155                 160
148 Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
149               165                 170                 175
151 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
152               180                 185                 190
154 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
155           195                 200                 205
157 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
158 210               215                 220
160 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
161 225               230                 235                 240
163 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
164           245                 250                 255
166 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
167           260                 265                 270
169 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
170           275                 280                 285
172 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
173       290                 295                 300
175 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
176 305               310                 315                 320
178 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
179           325                 330                 335
181 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
182           340                 345                 350
184 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
185       355                 360                 365
187 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
188       370                 375                 380
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191 <210> SEQ ID NO: 8
192 <211> LENGTH: 1152
193 <212> TYPE: DNA
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196 <220> FEATURE:
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199 <400> SEQUENCE: 8

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201 agcatggcga gcatggcaat gcacgtggcc cagcctgctg tggtactggc cagcagccga 120
202 ggcatcgcta gctttgtgtg tgagtatgca tctccaggca aatatactga ggtccgggtg 180
203 acagtgcttc ggcaggctga cagccaggtg actgaagtct gtgcggcaac ctacatgatg 240
204 gggaatgagt tgaccttcct agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
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206 gagctcatgt acccaccgcc atactacgag ggcataggca acggaaccca gatttatgta 420
207 attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
208 acatccccac cgtccccagc acctgaactc ctggggggat cgtcagtctt cctcttcccc 540
209 ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 600
210 gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 660
211 cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 720
212 gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 780
213 aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg cagccccga 840
214 gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 900
215 ctgacctgcc tggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960
216 gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1020
217 ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1080
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224 <212> TYPE: PRT
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234 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
235             20                  25                  30
237 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
238         35                  40                  45
240 Tyr Ala Ser Pro Gly Lys Tyr Thr Glu Val Arg Val Thr Val Leu Arg
241     50                  55                  60
243 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
244  65                  70                  75                  80
246 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
247                 85                  90                  95
249 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
250             100                 105                 110
252 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
253             115                 120                 125
255 Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
256     130                 135                 140
258 Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
259 145                 150                 155                 160
261 Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
262             165                 170                 175
264 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
265             180                 185                 190
267 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
268             195                 200                 205
270 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
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271     210                 215                 220
273 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
274 225                 230                 235                 240
276 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
277             245                 250                 255
279 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
280             260                 265                 270
282 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
283         275                 280                 285
285 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
286         290                 295                 300
288 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
289 305                 310                 315                 320
291 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
292             325                 330                 335
294 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
295             340                 345                 350
297 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
298         355                 360                 365
300 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
301         370                 375                 380
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VERIFICATION SUMMARY   DATE: 11/01/2001
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Input Set : **A:\Townsenl.app**
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